

Human Herpesvirus 8 Encodes a Homolog of Interleukin-6

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Received 17 September 1996/Accepted 8 October 1996

Kaposi's sarcoma is a multifocal lesion that is reported to be greatly influenced by cytokines such as interleukin-6 (IL-6) and oncostatin M. DNA sequences of a novel human gammaherpesvirus, termed human herpesvirus 8 (HHV-8) or Kaposi sarcoma-associated herpesvirus, have been identified in all epidemiological forms of Kaposi's sarcoma with high frequency. The presence of HHV-8 DNA is also clearly associated with certain B-cell lymphomas (body cavity-based lymphomas) and multicentric Castleman's disease. Sequence analysis of a 17-kb fragment revealed that adjacent to a block of conserved herpesvirus genes (major DNA-binding protein, glycoprotein B, and DNA polymerase), the genome of HHV-8 encodes structural homolog of IL-6. This cytokine is involved not only in the pathogenesis of Kaposi's sarcoma but also in certain B-cell lymphomas and multicentric Castleman's disease. The viral counterpart of IL-6 (vIL-6) has conserved important features such as cysteine residues involved in disulfide bridging or an amino-terminal signal peptide. Most notably, the region known to be involved in receptor binding is highly conserved in vIL-6. This conservation of essential features and the remarkable overlap between diseases associated with HHV-8 and diseases associated with IL-6 dysregulation clearly suggest that vIL-6 is involved in HHV-8 pathogenesis.

Kaposi's sarcoma (KS), a multifocal proliferative lesion of uncertain pathogenesis, is highly prevalent among homosexual AIDS patients. The originally described form (classical KS) occurs sporadically in some populations in eastern and southern Europe. KS is frequently found in central Africa, where the tumor occurs in young patients. The particular epidemiology among AIDS patients had suggested that an infectious agent other than human immunodeficiency virus is involved in KS pathogenesis. Studies with biopsy materials and cultured cells have indicated an important role for growth factors and cellular cytokines, such as basic fibroblast growth factor (35), interleukin-1 β (IL-1 β) (22), IL-6 (6, 19, 23, 25, 26, 33, 38), and oncostatin M (5, 7, 29, 32), for the proliferation of spindle cells in KS (24). Chang and colleagues (8) stirred considerable interest when they detected DNA sequences of a novel herpesvirus in KS tissues of AIDS patients. Meanwhile, DNA of this virus was consistently found in all epidemiological forms of KS (9, 11, 12, 18, 27, 31). The new virus, termed human herpesvirus 8 (HHV-8), shows marked sequence homology to herpesvirus saimiri, the prototype of gamma-2 herpesvirus; thus, HHV-8 appears to be the first human member of the gamma-2 herpesviruses (genus *Rhadinovirus*). Sequencing of a HHV-8 DNA fragment with a size of 20.7 kb indicated a genome organization that is collinear to herpesvirus saimiri, at least within an area of 17 open reading frames (ORFs) (28), which has been confirmed by sequence analysis of a further 50 kb (29a). Rhadinovirus genomes consist of a unique L-DNA that codes for 72 proteins (herpesvirus ateles) (1a) to 85 proteins (alcelaphine herpesvirus 1) (14a). The L-DNA is flanked by multirepetitive DNA that is high in GC content (H-DNA). Most strikingly, rhadinovirus genomes contain a surprisingly high number of genes that have apparently been acquired from

the host cell. They include the genes coding for enzymes involved in the nucleotide metabolism (thymidilate synthetase [17] and dihydrofolate reductase [DHFR] [36]) and complement-controlling proteins (CCPH [1] and CD59 [3]) and genes that could be involved in proliferation control, such as those encoding cyclins (20), the cytokine IL-17, and the IL-8 receptor (2). In the course of structural studies of the HHV-8 genome, we have now found a gene that encodes a structural equivalent of IL-6, providing the first known example of an IL-6-type gene in a viral genome.

DNA was extracted from a KS biopsy specimen, partially digested with the restriction endonuclease *Sau3A* (0.2 U/ μ g of DNA for 2 min), and enzymatically ligated with *Bam*HI-digested arms of the bacteriophage lambda DASHII (Stratagene, Inc., La Jolla, Calif.). Initially, this genomic library from KS tissue was screened with probes constructed according to the HHV-8 sequence information published by Chang and colleagues (8). HHV-8-positive lambda clones isolated by this method were sequenced using a shotgun approach (34), and terminal fragments were used as probes for further screening of the genomic library from KS tissue. Using the BLAST algorithm for amino acid comparisons (4), we found an ORF with significant homology to IL-6 (Fig. 1). The ORF for the viral homolog to IL-6 (vIL-6) has the coding capacity for a polypeptide of 204 amino acids (Fig. 2). It is located adjacent to a region with collinearity to the glycoprotein B/DNA polymerase block of herpesvirus saimiri. The reading frame to the left of vIL-6 is homologous to ORF11 of herpesvirus saimiri. Although vIL-6 is the positional analog of herpesvirus saimiri ORF12, these two genes are not homologous on the DNA or protein level. The HHV-8 reading frame to the left of vIL-6 encodes a gene with extensive homology to mammalian DHFR genes (29a), a gene that is also present in herpesvirus saimiri (Fig. 1). Interestingly, the DHFR gene of herpesvirus saimiri has a different genomic position: it is located close to the left end of the genome (ORF2). ORF13 of herpesvirus saimiri, which would be the positional analog of HHV-8 DHFR, encodes an unrelated protein with homology to IL-17. vIL-6 is

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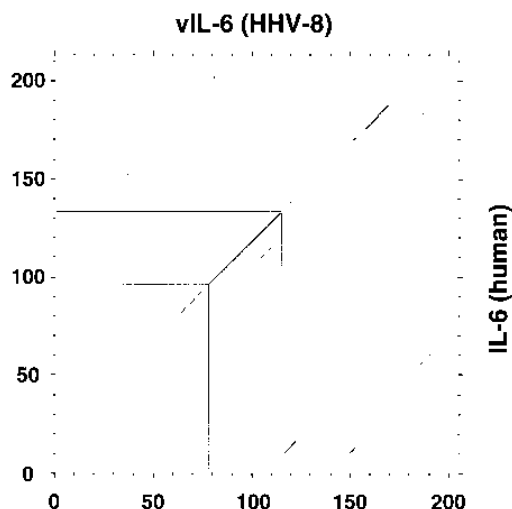


FIG. 3. Dot plot comparison of HHV-8 IL-6 (x axis) and human IL-6 (y axis). The dot plot comparison was calculated using the Genetics Computer Group suite of sequence analysis programs with the parameters for window and stringency set to 20 and 16, respectively. The well-conserved area, which is marked with continuous lines, is identical to the receptor-binding region of human IL-6 as identified by Ehlers et al. (13).

missing infectious agent was initially based on the detection of viral DNA only. HHV-8 DNA has been found in all epidemiological forms of KS in nearly 100% of cases, whereas DNA of this novel virus is infrequently seen in other tissue specimens and non-KS patients (9, 12, 18, 27). This finding is now supported for the first time by serological studies which show that HHV-8 occurs less frequently than most other human herpesviruses in the general population. However, the seroprevalence is high in groups at risk for the development of KS (16, 21). Detection of an IL-6 homolog in HHV-8 is highly suggestive that the respective viral gene product plays a functional role in the proliferation of typical KS cells. Two other disease conditions, Castleman's disease and body cavity-based lymphomas, have been found to be associated with the presence of HHV-8 DNA. A rare form of B-cell lymphoma in AIDS patients, body cavity-based lymphoma, invariably carries HHV-8 genomes in a latent state. Multicentric Castleman's disease is a chronic disease with benign hyperplastic lymphadenopathy. It is characterized by large lymph follicles with intervening plasma cells. The patients show marked hypergammaglobulinemia, and the B cells in such hyperplastic lymph nodes were found to produce large amounts of IL-6 by functional assays. Interestingly, in some patients, Castleman's disease may progress to multiple myeloma. Clinical improvement was associated with a decrease in serum IL-6 levels. Further studies are required to show whether functional assays are able to discriminate between cellular IL-6 and vIL-6. Based on DNA diagnostics, HHV-8 appears to be linked to three proliferative diseases, KS, body cavity-based B-cell lymphoma, and multicentric Castleman's disease, and a pathological role has been proposed for IL-6 in these diseases in the past, prior to the discovery of HHV-8. The identification of an IL-6 gene in HHV-8 thus supports the assumption that HHV-8 has a pathological role in these diseases and provides the basis for further investigation of its role in stimulating abnormal cellular proliferation.

Nucleotide sequence accession number. The vIL-6 sequence was submitted to GenBank and received accession number U73655.

This work was supported by Deutsche Krebshilfe, founded by Mildred Scheel, grant no. W134/94/F12.

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